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Interview with the Examiner Sitton, Bruce Grant and Tobey Tam on Thursday, May 8, 2008 at 11am EST.

Proposed claim amendments for US Application No. 10/723,681 (our reference SEQ-4069-UT):

1 (currently amended). A method for identifying a subject at risk of breast cancer, which comprises detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a human subject, wherein one or more polymorphic variations are detected ~~in one or more regions selected from a region between about~~ at one or more chromosome positions selected from the group consisting of chromosome positions 87330326, 87332557, 87332861, 87333099, 87333312, 87333569, 87341627, 87341722, and 87342924 ~~87330326 to about chromosome position 87342924, a region between about chromosome position 87352676 to about chromosome position 87369072, a region between about chromosome position 87311012 to about chromosome position 87314967 and a region between about chromosome position 87320287 to about chromosome position 87320855,~~ wherein each chromosome position is according to Build 33 of the GenBank database human genome sequence

whereby the ~~presence of the one or more polymorphic variations is indicative of the~~ subject is identified as being at risk of breast cancer based on the presence or absence of the one or more polymorphic variations associated with breast cancer.

2 (original). The method of claim 1, which further comprises obtaining the nucleic acid sample from the subject.

3-18 (cancelled).

19 (original) The method of claim 1, wherein detecting the presence or absence of the one or more polymorphic variations comprises:

hybridizing an oligonucleotide to the nucleic acid sample, wherein the oligonucleotide is complementary to a nucleotide sequence in the nucleic acid and hybridizes to a region adjacent to the polymorphic variation;

extending the oligonucleotide in the presence of one or more nucleotides, yielding extension products; and

detecting the presence or absence of a polymorphic variation in the extension products.

20-52 (cancelled).

53 (currently amended) A method for detecting or preventing breast cancer in a subject, which comprises:

detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a human subject, wherein one or more [[the]] polymorphic variations are [[is]] detected [[in]] at one or more ~~regions selected from a region between about~~ chromosome positions selected from the group consisting of chromosome positions 87330326, 87332557, 87332861, 87333099, 87333312, 87333569, 87341627, 87341722, and 87342924 ~~87330326 to about chromosome position 87342924, a region between about chromosome position 87352676 to about chromosome position 87369072, a region between about chromosome position 87311012 to about chromosome position 87314967 and a region between about chromosome position 87320287 to about chromosome position 87320855~~, wherein each chromosome position is according to Build 33 of the GenBank database human genome sequence and

administering a breast cancer prevention procedure or detection procedure to a subject identified as being at risk of breast cancer ~~in need thereof~~ based upon the presence or absence of the one or more polymorphic variations associated with breast cancer ~~in the nucleic acid sample~~.

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54 (cancelled).

55 (previously presented). The method of claim 53, wherein the breast cancer detection procedure is selected from the group consisting of a mammography, an early mammography program, a frequent mammography program, a biopsy procedure, a breast biopsy and biopsy from another tissue, a breast ultrasound and optionally ultrasound analysis of another tissue, breast magnetic resonance imaging (MRI) and optionally MRI analysis of another tissue, electrical impedance (T-scan) analysis of breast and optionally of another tissue, ductal lavage, nuclear medicine analysis scintimammography, *BRCA1* and/or *BRCA2* sequence analysis results, thermal imaging of the breast and optionally of another tissue, and a combination of the foregoing.

56 (withdrawn). The method of claim 53, wherein the breast cancer prevention procedure is selected from the group consisting of one or more selective hormone receptor modulators, one or more compositions that prevent production of hormones, one or more hormonal treatments, one or more biologic response modifiers, surgery, and drugs that delay or halt metastasis.

57 (withdrawn). The method of claim 56, wherein the selective hormone receptor modulator is selected from the group consisting of tamoxifen, reloxifene, and toremifene; the composition that prevents production of hormones is an aramotase inhibitor selected from the group consisting of exemestane, letrozole, anastrozol, groserelin, and megestrol; the hormonal treatment is selected from the group consisting of goserelin acetate and fulvestrant; the biologic response modifier is an antibody that specifically binds herceptin/HER2; the surgery is selected from the group consisting of lumpectomy and mastectomy; and the drug that delays or halts metastasis is pamidronate disodium.

58-87 (cancelled).

88 (new). The method of claim 1, wherein the one or more polymorphic variations comprise a polymorphic variation at position 87330326.

89 (new). The method of claim 1, wherein the one or more polymorphic variations comprise an adenine variation at position 87330326.

90 (new). The method of claim 1, wherein the one or more polymorphic variations comprise a polymorphic variation at position 87332557.

91 (new). The method of claim 1, wherein the one or more polymorphic variations comprise an adenine variation at position 87332557.

92 (new). The method of claim 1, wherein the one or more polymorphic variations comprise a polymorphic variation at position 87332861.

93 (new). The method of claim 1, wherein the one or more polymorphic variations comprise a cytosine variation at position 87332861.

94 (new). The method of claim 1, wherein the one or more polymorphic variations comprise a polymorphic variation at position 87333099.

95 (new). The method of claim 1, wherein the one or more polymorphic variations comprise a guanine variation at position 87333099.

96 (new). The method of claim 1, wherein the one or more polymorphic variations comprise a polymorphic variation at position 87333312.

97 (new). The method of claim 1, wherein the one or more polymorphic variations comprise a guanine variation at position 87333312.

98 (new). The method of claim 1, wherein the one or more polymorphic variations comprise a polymorphic variation at position 87333569.

99 (new). The method of claim 1, wherein the one or more polymorphic variations comprise a thymine variation at position 87333569.

100 (new). The method of claim 1, wherein the one or more polymorphic variations comprise a polymorphic variation at position 87341627.

101 (new). The method of claim 1, wherein the one or more polymorphic variations comprise an adenine variation at position 87341627.

102 (new). The method of claim 1, wherein the one or more polymorphic variations comprise a polymorphic variation at position 87341722.

103 (new). The method of claim 1, wherein the one or more polymorphic variations comprise a thymine variation at position 87341722.

104 (new). The method of claim 1, wherein the one or more polymorphic variations comprise a polymorphic variation at position 87342924.

105 (new). The method of claim 1, wherein the one or more polymorphic variations comprise a cytosine variation at position 87342924.

106 (new). The method of claim 53, wherein the one or more polymorphic variations comprise a polymorphic variation at position 87330326.

107 (new). The method of claim 53, wherein the one or more polymorphic variations comprise an adenine variation at position 87330326.

108 (new). The method of claim 53, wherein the one or more polymorphic variations comprise a polymorphic variation at position 87332557.

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109 (new). The method of claim 53, wherein the one or more polymorphic variations comprise an adenine variation at position 87332557.

110 (new). The method of claim 53, wherein the one or more polymorphic variations comprise a polymorphic variation at position 87332861.

111 (new). The method of claim 53, wherein the one or more polymorphic variations comprise a cytosine variation at position 87332861.

112 (new). The method of claim 53, wherein the one or more polymorphic variations comprise a polymorphic variation at position 87333099.

113 (new). The method of claim 53, wherein the one or more polymorphic variations comprise a guanine variation at position 87333099.

114 (new). The method of claim 53, wherein the one or more polymorphic variations comprise a polymorphic variation at position 87333312.

115 (new). The method of claim 53, wherein the one or more polymorphic variations comprise a guanine variation at position 87333312.

116 (new). The method of claim 53, wherein the one or more polymorphic variations comprise a polymorphic variation at position 87333569.

117 (new). The method of claim 53, wherein the one or more polymorphic variations comprise a thymine variation at position 87333569.

118 (new). The method of claim 53, wherein the one or more polymorphic variations comprise a polymorphic variation at position 87341627.

119 (new). The method of claim 53, wherein the one or more polymorphic variations comprise an adenine variation at position 87341627.

120 (new). The method of claim 53, wherein the one or more polymorphic variations comprise a polymorphic variation at position 87341722.

121 (new). The method of claim 53, wherein the one or more polymorphic variations comprise a thymine variation at position 87341722.

122 (new). The method of claim 53, wherein the one or more polymorphic variations comprise a polymorphic variation at position 87342924.

123 (new). The method of claim 53, wherein the one or more polymorphic variations comprise a cytosine variation at position 87342924.